

SEQUENCE LISTING

<110> Michael S.C. Fung
 Bill N.C. Sun
 Cecily R.Y. Sun

<120> Inhibitors of Complement Activation

<130> 98-2A

<150> 60/075,328

<151> 1998-02-20

<150> 09/253,689

<151> 1999-02-20

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 699

<212> DNA

<213> human

<220>

<221> CDS

<222> (4)...(687)

<400> 1

cgg atc ctg ggc ggc aga gag gcc gag gcg cac gcg cgg ccc tac atg 48
 Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met
 1 5 10 15

gcg tcg gtg cag ctg aac ggc gcg cac ctg tgc ggc ggc gtc ctg gtg 96
 Ala Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val
 20 25 30

gcg gag cag tgg gtg ctg agc gcg gcg cac tgc ctg gag gac gcg gcc 144
 Ala Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala
 35 40 45

gac ggg aag gtg cag gtt ctc ctg ggc gcg cac tcc ctg tcg cag ccg 192
 Asp Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
 50 55 60

gag ccc tcc aag cgc ctg tac gac gtg ctc cgc gca gtg ccc cac ccg 240
 Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
 65 70 75

gac agc cag ccc gac acc atc gac cac gac ctc ctg ctg cta cag ctg 288
 Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Gln Leu

80	85	90	95	
tcg gag aag gcc aca ctg ggc cct gct gtg cgc ccc ctg ccc tgg cag				336
Ser Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln				
100	105	110		
cgc gtg gac cgc gac gtg gca ccg gga act ctc tgc gac gtg gcc ggc				384
Arg Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly				
115	120	125		
tgg ggc ata gtc aac cac gcg ggc cgc cgc ccg gac agc ctg cag cac				432
Trp Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His				
130	135	140		
gtg ctc ttg cca gtg ctg gac cgc gcc acc tgc aac cgg cgc acg cac				480
Val Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His				
145	150	155		
cac gac ggc gcc atc acc gag cgc ttg atg tgc gcg gag agc aat cgc				528
His Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg				
160	165	170	175	
cgg gac agc tgc aag ggt gac tcc ggg ggc ccg ctg gtg tgc ggg ggc				576
Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly				
180	185	190		
gtg ctc gag ggc gtg gtc acc tcg ggc tcg cgc gtt tgc ggc aac cgc				624
Val Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg				
195	200	205		
aag aag ccc ggg atc tac acc cgc gtg gcg agc tat gcg gcc tgg atc				672
Lys Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile				
210	215	220		
gac agc gtc ctg gcc tagtaggaat tc				699
Asp Ser Val Leu Ala				
225				
<210> 2				
<211> 228				
<212> PRT				
<213> human				
<400> 2				
Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met Ala				
1	5	10	15	
Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val Ala				
20	25	30		
Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala Asp				
35	40	45		
Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu				
50	55	60		
Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp				
65	70	75	80	

Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Gln Leu Ser
85 90 95
Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln Arg
100 105 110
Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly Trp
115 120 125
Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His Val
130 135 140
Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His His
145 150 155 160
Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg Arg
165 170 175
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
180 185 190
Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
195 200 205
Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile Asp
210 215 220
Ser Val Leu Ala
225

<210> 3

<211> 714

<212> DNA

<213> pig

<220>

<221> CDS

<222> (4)...(702)

<400> 3

cgg atc ctg ggt ggc cag gag gcc aag tcc cac gag aga ccc tac atg 48
Ile Leu Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met
1 5 10 15

gca tgc gtg cag gtg aac ggc aag cac gtg tgc gga ggc ttc ctg gtg 96
Ala Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val
20 25 30

tct gag cag tgg gtg ctg agt gca gca cac tgc ctg gag gac gtg gcc 144
Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala
35 40 45

gag ggg aag ctg cag gtt ctc ctg ggt gcg cac tcc ctg tca cag ccc 192
Glu Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
50 55 60

gag ccc tgc aag cgc ctg tac gac gtg ctc cgc gcc gtg ccc cac cca 240
Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
65 70 75

gac agc cag cct gac acc atc gac cat gat ctc ctc ctg ctg aag ctc 288
Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Lys Leu
80 85 90 95

tcc gag aag gcc gag ctg ggc cct gcc gtg cag ccc ctt gcc tgg caa 336
 Ser Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln
 100 105 110

cga gag gac cac gag gtt ccg gca ggc acg ctc tgc gac gtg gcc ggc 384
 Arg Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly
 115 120 125

tgg gga gtg gtc agt cac act ggc cgc cgg ccc gac cgt ctg cag cac 432
 Trp Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His
 130 135 140

ctg ctc cta ccg gtg ctg gac cgc acc acc tgc aac ctg cgc aca tac 480
 Leu Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr
 145 150 155

cac gat ggc acc atc acc gag cgc atg atg tgc gcg gag agc aac cgt 528
 His Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg
 160 165 170 175

cgg gac agc tgc aag ggc gac tcc gga ggc ccg ctg gtg tgc ggg ggt 576
 Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
 180 185 190

gtg gcc gag gga gtg gtt acc tca ggc tcc cga gtc tgc ggc aac cgc 624
 Val Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
 195 200 205

aag aaa ccc ggc atc tac acg cgc ttg gcg agc tac gtg gcc tgg atc 672
 Lys Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile
 210 215 220

gac gga gtg atg gct gac agc gca gcc gcc tagtaggaat tc 714
 Asp Gly Val Met Ala Asp Ser Ala Ala Ala
 225 230

<210> 4
 <211> 233
 <212> PRT
 <213> pig

<400> 4
 Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met Ala
 1 5 10 15
 Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val Ser
 20 25 30
 Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala Glu
 35 40 45
 Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
 50 55 60
 Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
 65 70 75 80
 Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Lys Leu Ser
 85 90 95

Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln Arg
 100 105 110
 Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly Trp
 115 120 125
 Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His Leu
 130 135 140
 Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr His
 145 150 155 160
 Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg Arg
 165 170 175
 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
 180 185 190
 Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
 195 200 205
 Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile Asp
 210 215 220
 Gly Val Met Ala Asp Ser Ala Ala Ala
 225 230

<210> 5
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer

<400> 5
 tgcggccgct gtaggtgctg tcttt 25

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 6
 ggaattcact cggtattctc gga 23

<210> 7
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 7
 tccgagaata acgagtg 17

<210> 8
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 8

cattgaaagc tttgggtag aagttgttc

29

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

cgcgccgca gctgctcaga gtgtaga

27

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10

cggtagctt cactggctca gggaaata

28

<210> 11

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

aagaagcttg ccgccacat ggattggctg tggaact

37

<210> 12

<211> 31

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 12

cgggatcctc aaactttctt gtccaccttg g

31

<210> 13

<211> 36

<212> DNA

1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398</
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	--------

<223> primer

aagaaagctt gccgccacca tgttctcact agctct

36

<211> 26

<213> Artificial Sequence

<223> primer

cgggatcctt ctccctctaa cactct

26

<211> 9

<213> human

Glu Pro Lys Ser Cys Asp Lys Thr His

1 5